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OM nucleic - nucleic search, using sw model

Run on: July 28, 2004, 06:14:15 ; Search time 16680 Seconds
                                           (without alignments)
                                           11529.559 Million cell updates/sec

Title: US-09-753-143-72
Perfect score: 4437
Sequence: 1 GCGCGGCGGCCGTGGTTGCG..........AAAAAAAAAAAAAAAAAAAA 4437

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                  1:   gb_ba:*
                  2:   gb_htg:*
                  3:   gb_in:*
                  4:   gb_om:*
                  5:   gb_ov:*
                  6:   gb_pat:*
                  7:   gb_ph:*
                  8:   gb_pl:*
                  9:   gb_pr:*
                  10: gb_ro:*
                  11: gb_sts:*
                  12: gb_sy:*
                  13: gb_un:*
                  14: gb_vi:*
                  15: em_ba:*
                  16: em_fun:*
                  17: em_hum:*
                  18: em_in:*
                  19: em_mu:*
                  20: em_om:*
                  21: em_or:*
                  22: em_ov:*
                  23: em_pat:*
                  24: em_ph:*
                  25: em_pl:*
                  26: em_ro:*
                  27: em_sts:*

```
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Parent

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	4437	100.0	4437	6	AR049083 _USPN 5824501_	AR049083 Sequence
	2	4435.4	100.0	4437	6	AR211947 " _6399378_	AR211947 Sequence
	3	4435.4	100.0	4437	6	AX335489 _WO 01/94629_	AX335489 Sequence
	4	4435.4	100.0	4437	6	AX695780 _WO 03/08583_	AX695780 Sequence
	5	4435.4	100.0	4437	9	HSU39817 _—GenBank_	U39817 Human Bloom
	6	4252.4	95.8	4254	6	AX695781	AX695781 Sequence
	7	2925.8	65.9	4498	6	AX695777	AX695777 Sequence
	8	2925.8	65.9	4498	10	MMBLM	_GenBank—_ Z98263 _Mus_ musculu
	9	2888	65.1	4763	10	AB008674	" _—AB008674_ _Mus_ muscu
	10	2882.6	65.0	4251	6	AX695778	AX695778 Sequence
	11	1204.2	27.1	3581	5	AB040747	_GB—_ AB040747 _Gallus_ ga
	12	1082.8	24.4	4124	5	AF307841	AF307841 Xenopus 1
c	13	704	15.9	95565	9	AC000379	_GB—_ AC000379 _human_ Chr _1997_
	14	704	15.9	96594	6	AX695779	AX695779 Sequence
	15	704	15.9	99500	6	AR211954	AR211954 Sequence
	16	704	15.9	147854	9	AC021422	AC021422 Homo sapi
c	17	704	15.9	157248	9	AC002312	AC002312 Human Chr
c	18	670.4	15.1	100259	9	AC005800	AC005800 Homo sapi
	19	670.4	15.1	142201	9	AC124248	AC124248 Homo sapi
c	20	558.8	12.6	64525	2	AC124238	AC124238 Homo sapi
	21	534	12.0	630	6	AR211955	AR211955 Sequence
	22	460.8	10.4	514	9	BC062697	BC062697 Homo sapi
c	23	450.6	10.2	198446	2	AC110907	AC110907 Mus muscu
c	24	441.2	9.9	94175	2	AC136849	AC136849 Rattus no
	25	425.6	9.6	96593	6	AX695776	AX695776 Sequence
	26	359.6	8.1	260924	2	AC095740	AC095740 Rattus no
	27	335.6	7.6	4835	3	DMU92536	U92536 Drosophila
	28	305.4	6.9	3172	3	AY095296	AY095296 Caenorhab
	29	299.2	6.7	2060	8	ATH404470	AJ404470 Arabidops
	30	269.2	6.1	3567	8	BT010133	BT010133 Arabidops
	31	269.2	6.1	3891	8	AY120761	AY120761 Arabidops
	32	269.2	6.1	3916	8	ATH404473	AJ404473 Arabidops
	33	268	6.0	5161	8	SPDNAHELG	Y09426 S.pombe hus

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OM nucleic - nucleic search, using sw model
Run on: July 28, 2004, 06:09:25 ; Search time 1584 Seconds
                                           (without alignments)
                                           11899.782 Million cell updates/sec
Title: US-09-753-143-72
Perfect score: 4437
Sequence: 1 GCGCGGCGGCCGTGGTTGCG..........AAAAAAAAAAAAAAAAAAAA 4437
Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0
Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
Database :   N_Geneseq_29Jan04:*
                  1: geneseqn1980s:*
                  2: geneseqn1990s:*
                  3: geneseqn2000s:*
                  4: geneseqn2001as:*
                  5: geneseqn2001bs:*
                  6: geneseqn2002s:*
                  7: geneseqn2003as:*
                  8: geneseqn2003bs:*
                  9: geneseqn2003cs:*
                  10: geneseqn2004s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

              %
Result   Query
  No.   Score Match Length DB ID   Description
----
    1 4435.4 100.0 4437 6   ABL67661 WO 01/194629   Abl67661 Oesophagu
    2 4435.4 100.0 4437 6   AAD41733 USPN 6399378   Aad41733 Human REC
    3 4435.4 100.0 4437 8   ADA02889 WO 03/057146   Ada02889 Human BLM
    4 4435.4 100.0 4437 9   ADB72627 WO 02/005853   Adb72627 Human BLM   App.
    5 4435.4 100.0 4437 9   ADC85368 WO 03/045230   Adc85368 Human Blm
    6 4432.2 99.9 4437 2   AAT67013 WO 97/17979   Aat67013 Bloom syn
    7 4430.6 99.9 4437 2   AAT93390   Aat93390 Bloom's s
    8 4430.6 99.9 4437 2   AAT93392   Aat93392 Bloom's s
    9 4430.6 99.9 4437 2   AAT93395   Aat93395 Bloom's s
   10 4430.6 99.9 4437 2   AAT93394   Aat93394 Bloom's s
   11 4421.2 99.6 4438 2   AAT93391   Aat93391 Bloom's s
   12 4416.2 99.5 4434 2   AAT93389   Aat93389 Bloom's s
   13 4414.8 99.5 4438 2   AAT93393   Aat93393 Bloom's s
   14 4252.4 95.8 4254 8   ADA02890 WO 03/057146   Ada02890 Human BLM
   15 4252.4 95.8 4254 9   ADB72628   Adb72628 Human BLM
   16 4252.4 95.8 4254 9   ADC85369   Adc85369 Human Blm
   17 2925.8 65.9 4498 8   ADA02886   Ada02886 Mouse Blm

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OM nucleic - nucleic search, using sw model

Run on: July 28, 2004, 00:56:19 ; Search time 289 Seconds
                                          (without alignments)
                                          8520.128 Million cell updates/sec

Title: US-09-753-143-72
Perfect score: 4437
Sequence: 1 GCGCGGCGGCCGTGGTTGCG..........AAAAAAAAAAAAAAAAAAAA 4437

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES
                     %
Result   Query
    No.   Score Match Length DB   ID   Description
----
      1   4437   100.0   4437 1   US-08-559-303B-72   Sequence 72, Appl
      2   4437   100.0   4437 3   US-09-175-828-72   Sequence 72, Appl
      3 4435.4   100.0   4437 4   US-09-798-096-3   Sequence 3, Appli
      4   704   15.9 99500 4   US-09-798-096-10   Sequence 10, Appl
      5   534   12.0   630 4   US-09-798-096-11   Sequence 11, Appl
      6   159.8   3.6   1926 4   US-09-543-681A-187   Sequence 187, App
      7   129   2.9 1830121 4   US-09-557-884-1   Sequence 1, Appli
      8   129   2.9 1830121 4   US-09-643-990A-1   Sequence 1, Appli
      9   123.6   2.8   1851 4   US-09-107-532A-3604   Sequence 3604, Ap
     10   120.6   2.7   1914 4   US-09-134-001C-2821   Sequence 2821, Ap
c   11   119.2   2.7   2004 4   US-08-956-171E-269   Sequence 269, App
     12   113.6   2.6   1860 4   US-09-489-039A-904   Sequence 904, App

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OM nucleic - nucleic search, using sw model

Run on: July 28, 2004, 05:30:25 ; Search time 1843 Seconds
                                          (without alignments)
                                          11804.250 Million cell updates/sec

Title: US-09-753-143-72
Perfect score: 4437
Sequence: 1 GCGCGGCGGCCGTGGTTGCG..........AAAAAAAAAAAAAAAAAAAA 4437

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
                 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4437	100.0	4437	9	US-09-753-143-72	Sequence 72, Appl
2	4435.4	100.0	4437	9	US-09-962-832-112	Sequence 112, App
3	4435.4	100.0	4437	12	US-09-997-722-155	Sequence 155, App
4	4435.4	100.0	4437	13	US-10-342-887-420	Sequence 420, App
5	4435.4	100.0	4437	13	US-10-172-118-420	Sequence 420, App
6	4313.4	97.2	4544	16	US-10-062-674-1885	Sequence 1885, Ap
7	4252.4	95.8	4254	12	US-09-997-722-156	Sequence 156, App
8	2925.8	65.9	4498	12	US-09-997-722-152	Sequence 152, App
9	2882.6	65.0	4251	12	US-09-997-722-153	Sequence 153, App
10	704	15.9	96594	12	US-09-997-722-154	Sequence 154, App
c 11	701	15.8	701	15	US-10-029-386-20899	Sequence 20899, A
c 12	581.4	13.1	607	9	US-09-867-701-10217	Sequence 10217, A
13	425.6	9.6	96593	12	US-09-997-722-151	Sequence 151, App
14	380	8.6	509	16	US-10-062-674-1166	Sequence 1166, Ap
c 15	306	6.9	306	9	US-09-864-761-22841	Sequence 22841, A
16	273.4	6.2	2150	13	US-10-425-114-19444	Sequence 19444, A
17	254.2	5.7	1584	13	US-10-425-114-3024	Sequence 3024, Ap
18	250.2	5.6	2925	10	US-09-793-807-3	Sequence 3, Appli
19	246.4	5.6	1952	17	US-10-437-963-38862	Sequence 38862, A
20	245.4	5.5	567	10	US-09-918-995-28609	Sequence 28609, A
21	241	5.4	2505	13	US-10-425-114-470	Sequence 470, App
c 22	206.6	4.7	365	9	US-09-864-761-5348	Sequence 5348, Ap
c 23	206.6	4.7	365	9	US-09-864-761-14448	Sequence 14448, A
24	204.6	4.6	5868	15	US-10-293-504-2	Sequence 2, Appli
c 25	179.8	4.1	558	15	US-10-029-386-7199	Sequence 7199, Ap
26	172	3.9	6916	15	US-10-293-504-1	Sequence 1, Appli
27	166.2	3.7	1172	13	US-10-282-122A-25257	Sequence 25257, A
28	161.4	3.6	1800	13	US-10-282-122A-33030	Sequence 33030, A
29	160.6	3.6	2160	13	US-10-282-122A-12367	Sequence 12367, A
30	154.8	3.5	1340	13	US-10-424-599-78917	Sequence 78917, A
31	154.4	3.5	1164	13	US-10-424-599-35459	Sequence 35459, A
32	148.2	3.3	1863	13	US-10-282-122A-40794	Sequence 40794, A
33	143.8	3.2	684707	16	US-10-398-221-9	Sequence 9, Appli
c 34	143.8	3.2	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
35	143.2	3.2	1803	13	US-10-282-122A-12144	Sequence 12144, A
36	142.6	3.2	2481	13	US-10-282-122A-16967	Sequence 16967, A
37	142.4	3.2	2127	13	US-10-282-122A-16639	Sequence 16639, A
38	139.6	3.1	2145	13	US-10-282-122A-15954	Sequence 15954, A
39	137.2	3.1	1833	13	US-10-282-122A-41841	Sequence 41841, A
40	137	3.1	2301	13	US-10-282-122A-29918	Sequence 29918, A
41	136.6	3.1	1860	9	US-09-815-242-6988	Sequence 6988, Ap
42	136.6	3.1	1860	13	US-10-282-122A-22087	Sequence 22087, A
c 43	135.4	3.1	2731748	17	US-10-297-465A-1	Sequence 1, Appli
44	134.6	3.0	1848	13	US-10-282-122A-38789	Sequence 38789, A
45	133	3.0	1830	13	US-10-282-122A-39599	Sequence 39599, A

ALIGNMENTS

RESULT 1
US-09-753-143-72

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OM nucleic - nucleic search, using sw model

Run on: July 28, 2004, 09:58:50 ; Search time 10409 Seconds
                                          (without alignments)
                                          12729.224 Million cell updates/sec

Title: US-09-753-143-72
Perfect score: 4437
Sequence: 1 GCGCGGCGGCCGTGGTTGCG..........AAAAAAAAAAAAAAAAAAAA 4437

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*
                 28: gb_gss1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4364.2	98.4	4493	11	BC034480 (2002)	BC034480 Homo sapi
c 2	947.8	21.4	974	9	AL556823	AL556823 AL556823
3	942	21.2	1019	9	AL556853	AL556853 AL556853
4	810.4	18.3	868	12	BM451903	BM451903 AGENCOURT
5	803	18.1	964	12	BG199179	BG199179 RST18458
c 6	781.8	17.6	849	13	BX434842	BX434842 BX434842
7	776.4	17.5	874	13	BX451969	BX451969 BX451969
8	726.6	16.4	882	12	BI091601	BI091601 602859024
9	711	16.0	772	12	BG772975	BG772975 602721230
10	709.8	16.0	873	13	BX451970	BX451970 BX451970
11	697	15.7	865	13	BQ230262	BQ230262 AGENCOURT
12	695.4	15.7	697	12	BI091772	BI091772 602858823
c 13	683	15.4	784	12	BM041661	BM041661 603614723
14	680.2	15.3	782	14	CF748661	CF748661 UI-M-HJ0-
15	679.6	15.3	792	12	BM040993	BM040993 603614723
c 16	673.4	15.2	688	12	BG875917	BG875917 IL3-CT021
17	669.6	15.1	955	12	BM542461	BM542461 AGENCOURT
18	659.4	14.9	774	14	CA317178	CA317178 UI-M-FW0-
19	646	14.6	724	12	BG574669	BG574669 602596672
c 20	642.4	14.5	772	14	CB243435	CB243435 UI-CF-FN0
21	629.4	14.2	801	12	BI685028	BI685028 603310006
22	610.4	13.8	665	10	BE538092	BE538092 601062725
23	609	13.7	648	12	BG721596	BG721596 602695720
24	608	13.7	734	12	BI656900	BI656900 603284510
25	607.4	13.7	638	12	BI667071	BI667071 603291250
26	603.6	13.6	861	12	BI691674	BI691674 603307363
27	596.8	13.5	664	14	CD707743	CD707743 EST24270
28	596.6	13.4	691	10	BE618504	BE618504 601462944
29	595.6	13.4	1201	13	BX419085	BX419085 BX419085
30	584.4	13.2	610	13	BX643048	BX643048 DKFZp781H
c 31	581.4	13.1	607	9	AI590599	AI590599 tw23d07.x
32	580.8	13.1	1061	12	BG397477	BG397477 602439306
33	579.4	13.1	960	12	BG756262	BG756262 602713574
34	568	12.8	617	14	CD698394	CD698394 EST14917
35	567.2	12.8	825	14	CF411420	CF411420 CH3#073_E
36	564.8	12.7	575	10	AW502890	AW502890 UI-HF-BN0
37	559.6	12.6	1090	12	BM804157	BM804157 AGENCOURT
38	558	12.6	610	13	BX475196	BX475196 DKFZp686I
39	547.4	12.3	693	10	BE535950	BE535950 601062268
40	541	12.2	564	13	BX474261	BX474261 DKFZp686J
41	535.2	12.1	977	10	BE889560	BE889560 601512475
42	534	12.0	630	9	AI114820	AI114820 HA1429 Hu
43	516.8	11.6	523	13	BX106802	BX106802 BX106802
44	514.8	11.6	531	9	AL120858	AL120858 DKFZp762J
c 45	514.2	11.6	747	10	BE963549	BE963549 601657344